

PATENT

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IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Inventors: Steven COLLIVER *et al.*)
)
U.S. National Phase of PCT/EP03/01465) Art Unit: Not Assigned
)
International Filing Date: February 13, 2003) Examiner: Not Assigned
)
For: NUTRITIONALLY ENHANCED PLANTS)

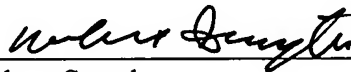
Commissioner for Patents
Washington, D.C. 20231

STATEMENT ACCOMPANYING SEQUENCE LISTING

The undersigned hereby states upon information and belief that the Sequence Listing submitted concurrently herewith does not include matter which goes beyond the content of the application as filed and that the information recorded on the diskette submitted concurrently herewith is identical to the written Sequence Listing submitted herewith.

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SEQUENCE LISTING

<110> COLLIVER, Steven Peter
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 van der HIJDEN, Hendrikus Theodorus Wilhelmus Maria

<120> PRODUCTION OF DADZEIN IN TRANSGENIC PLANTS

<130> 56159-5241

<150> PCT/EP03/01465
 <151> 2003-02-13

<150> EP 02251404.6
 <151> 2002-02-28

<160> 59

<170> PatentIn version 3.2

<210> 1
 <211> 946
 <212> DNA
 <213> Pisum sativum

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 ctgacaaagg aggatcatga gaaaattgat caaattaagc agaatcgttt gatccctgga 900
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<210> 2
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 <212> PRT
 <213> Pisum sativum

<400> 2

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Gln Ile Lys Met Pro Val Val Gly Met Gly Ser Ala Pro Asp Phe Thr
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Cys Lys Lys Asp Thr Lys Glu Ala Ile Ile Glu Ala Ile Lys Gln Gly
 35 40 45

Tyr Arg His Phe Asp Thr Ala Ala Ala Tyr Gly Ser Glu Gln Ala Leu
 50 55 60

Gly Glu Ala Leu Asn Glu Ala Ile Gln Leu Gly Leu Val Thr Arg Glu
 65 70 75 80

Gln Leu Phe Val Thr Ser Lys Leu Trp Val Thr Glu Asn His Pro His
 85 90 95

Leu Val Leu Pro Ala Leu Gln Lys Ser Leu Lys Thr Leu Gln Leu Asp
 100 105 110

Tyr Leu Asp Leu Tyr Leu Ile His Trp Pro Leu Ser Ser Gln Pro Gly
 115 120 125

Lys Phe Ser Phe Pro Ile Asp Val Ala Asp Leu Leu Pro Phe Asp Val
 130 135 140

Lys Gly Val Trp Glu Ser Met Glu Glu Ala Leu Arg Leu Gly Leu Thr
 145 150 155 160

Lys Ala Ile Gly Val Ser Asn Phe Ser Val Lys Lys Leu Gln Lys Leu
 165 170 175

Leu Ser Val Ala Thr Val Leu Pro Ala Val Asn Gln Val Glu Met Asn
 180 185 190

Leu Ala Trp Gln Gln Lys Lys Leu Arg Glu Phe Cys Asn Glu Asn Gly
195 200 205

Ile Val Leu Thr Ala Phe Ser Pro Leu Arg Lys Gly Ala Ser Arg Gly
210 215 220

Ala Asn Glu Val Met Glu Asn Asp Met Leu Lys Gln Ile Ala Asp Ala
225 230 235 240

His Gly Lys Ser Ile Ala Gln Ile Ser Leu Arg Trp Leu Tyr Glu Gln
245 250 255

Gly Ile Thr Phe Val Pro Lys Ser Tyr Asp Lys Glu Arg Met Ser Gln
260 265 270

Asn Leu Arg Ile Phe Asp Trp Thr Leu Thr Lys Glu Asp His Glu Lys
275 280 285

Ile Asp Gln Ile Lys Gln Asn Arg Leu Ile Pro Gly Pro Thr Lys Pro
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Ser Leu Asn Asp Leu Trp Asp Asp Glu Ile
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<211> 1567
<212> DNA
<213> Glycine max

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<210> 4
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<212> PRT
<213> Glycine max

<400> 4

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20 25 30

Pro Asn Pro Pro Ser Pro Lys Pro Arg Leu Pro Phe Ile Gly His Leu
35 40 45

His Leu Leu Lys Asp Lys Leu Leu His Tyr Ala Leu Ile Asp Leu Ser
50 55 60

Lys Lys His Gly Pro Leu Phe Ser Leu Tyr Phe Gly Ser Met Pro Thr
65 70 75 80

Val Val Ala Ser Thr Pro Glu Leu Phe Lys Leu Phe Leu Gln Thr His
85 90 95

Glu Ala Thr Ser Phe Asn Thr Arg Phe Gln Thr Ser Ala Ile Arg Arg
100 105 110

Leu Thr Tyr Asp Ser Ser Val Ala Met Val Pro Phe Gly Pro Tyr Trp
115 120 125

Lys Phe Val Arg Lys Leu Ile Met Asn Asp Leu Leu Asn Ala Thr Thr
130 135 140

Val Asn Lys Leu Arg Pro Leu Arg Thr Gln Gln Thr Arg Lys Phe Leu
145 150 155 160

Arg Val Met Ala Gln Gly Ala Glu Ala Gln Lys Pro Leu Asp Leu Thr
165 170 175

Glu Glu Leu Leu Lys Trp Thr Asn Ser Thr Ile Ser Met Met Met Leu
180 185 190

Gly Glu Ala Glu Glu Ile Arg Asp Ile Ala Arg Glu Val Leu Lys Ile
195 200 205

Phe Gly Glu Tyr Ser Leu Thr Asp Phe Ile Trp Pro Leu Lys His Leu
210 215 220

Lys Val Gly Lys Tyr Glu Lys Arg Ile Asp Asp Ile Leu Asn Lys Phe
225 230 235 240

Asp Pro Val Val Glu Arg Val Ile Lys Lys Arg Arg Glu Ile Val Arg
245 250 255

Arg Arg Lys Asn Gly Glu Val Val Glu Gly Glu Val Ser Gly Val Phe
260 265 270

Leu Asp Thr Leu Leu Glu Phe Ala Glu Asp Glu Thr Met Glu Ile Lys
275 280 285

Ile Thr Lys Asp His Ile Lys Gly Leu Val Val Asp Phe Phe Ser Ala
290 295 300

Gly Thr Asp Ser Thr Ala Val Ala Thr Glu Trp Ala Leu Ala Glu Leu
305 310 315 320

Ile Asn Asn Pro Lys Val Leu Glu Lys Ala Arg Glu Glu Val Tyr Ser
325 330 335

Val Val Gly Lys Asp Arg Leu Val Asp Glu Val Asp Thr Gln Asn Leu
340 345 350

Pro Tyr Ile Arg Ala Ile Val Lys Glu Thr Phe Arg Met His Pro Pro
355 360 365

Leu Pro Val Val Lys Arg Lys Cys Thr Glu Glu Cys Glu Ile Asn Gly
370 375 380

Tyr Val Ile Pro Glu Gly Ala Leu Ile Leu Phe Asn Val Trp Gln Val
385 390 395 400

Gly Arg Asp Pro Lys Tyr Trp Asp Arg Pro Ser Glu Phe Arg Pro Glu
405 410 415

Arg Phe Leu Glu Thr Gly Ala Glu Gly Glu Ala Gly Pro Leu Asp Leu
420 425 430

Arg Gly Gln His Phe Gln Leu Leu Pro Phe Gly Ser Gly Arg Arg Met
435 440 445

Cys Pro Gly Val Asn Leu Ala Thr Ser Gly Met Ala Thr Leu Leu Ala
450 455 460

Ser Leu Ile Gln Cys Phe Asp Leu Gln Val Leu Gly Pro Gln Gly Gln
465 470 475 480

Ile Leu Lys Gly Gly Asp Ala Lys Val Ser Met Glu Glu Arg Ala Gly
485 490 495

Leu Thr Val Pro Arg Ala His Ser Leu Val Cys Val Pro Leu Ala Arg
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Ile Gly Val Ala Ser Lys Leu Leu Ser
515 520

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<211> 670
<212> DNA
<213> Lotus corniculatus

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gaggggaagt tcataaaatt cactggcata ggagtgtatt tggaagatac agcagtggat 180
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aaggtggatt ttccaccagg ttcctctggt ttctaccgac aatcaacaga tggaaaatta 480
gggcttagtt tctctttgga tgacacgata ccagaagaag aggctgtagt tatagagaac 540
aaggcactct cagaggcagt gttagagacc atgattggcg agcatgctgt ttcccctgat 600
ttgaagcggt gtttggctga aaggttgcct attgtgatga accaggggtct tctcctcact 660
ggaaactgat 670

<210> 6
<211> 222
<212> PRT
<213> Lotus corniculatus

<400> 6

Met Ala Ala Ser Leu Thr Pro Ile Gln Val Glu Asn Leu Gln Phe Pro
1 5 10 15

Ala Ser Val Thr Ser Pro Ala Thr Ala Lys Ser Tyr Phe Leu Gly Gly
20 25 30

Ala Gly Glu Arg Gly Leu Thr Ile Glu Gly Lys Phe Ile Lys Phe Thr
35 40 45

Gly Ile Gly Val Tyr Leu Glu Asp Thr Ala Val Asp Ser Leu Ala Thr
50 55 60

Lys Trp Lys Gly Lys Ser Ser Gln Glu Leu Gln Asp Ser Leu Asp Phe
65 70 75 80

Phe Arg Asp Ile Ile Ser Ser Pro Ser Glu Lys Leu Ile Arg Gly Ser
85 90 95

Lys Leu Arg Pro Leu Ser Gly Val Glu Tyr Ser Arg Lys Val Met Glu
100 105 110

Asn Cys Val Ala His Met Lys Ser Ala Gly Thr Tyr Gly Glu Ala Glu
115 120 125

Ala Thr Ala Ile Glu Lys Phe Ala Glu Ala Phe Arg Lys Val Asp Phe
130 135 140

Pro Pro Gly Ser Ser Val Phe Tyr Arg Gln Ser Thr Asp Gly Lys Leu
145 150 155 160

Gly Leu Ser Phe Ser Leu Asp Asp Thr Ile Pro Glu Glu Glu Ala Val
165 170 175

Val Ile Glu Asn Lys Ala Leu Ser Glu Ala Val Leu Glu Thr Met Ile
180 185 190

Gly Glu His Ala Val Ser Pro Asp Leu Lys Arg Cys Leu Ala Glu Arg
195 200 205

Leu Pro Ile Val Met Asn Gln Gly Leu Leu Leu Thr Gly Asn
210 215 220

<210> 7

<211> 9

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence: conserved
regions of various known CHR's

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<210> 8

<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:conserved
regions of various known CHR's

<400> 8

Ala Ile Ile Glu Ala Ile Lys Gln
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<210> 9
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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 9
atggttgctgg aacttgca t 21

<210> 10
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<212> DNA
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<223> Description of Artificial Sequence:primer

<400> 10
ttagaaagga gtttagatgc aacg 24

<210> 11
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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 11
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<210> 12
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<213> Artificial Sequence

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<400> 12
ccgataccttg caagtggaac ac 22

<210> 13
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<223> Description of Artificial Sequence:primer

<400> 13
ttgtccagat agcccagtag ctg 23

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<210> 15
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<210> 16
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<400> 17
ggaaacagct atgaccatga ttac 24

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<400> 18
aaggatccgt cgacatc 17

<210> 19
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<400> 19
agtccccat ggtacgtcct gtagaaacc 29

<210> 20
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<400> 20
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<210> 22

<211> 17
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<400> 22
gacatcgata atacgac 17

<210> 23
<211> 24
<212> DNA
<213> Artificial Sequence

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<400> 23
tgctacctct agagaatttc cccg 24

<210> 24
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<212> DNA
<213> Artificial Sequence

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<400> 24
ctaagcccct aagtattcca tcaggtgatt 30

<210> 25
<211> 34
<212> DNA
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<400> 25
ccaggtggaa aattacacat gtgcttgaaa gagc 34

<210> 26
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<400> 26
tttgaaaagt ctaataacga gggtcagaag 30

<210> 27
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<400> 27
tactcaagga aggttgatgg agaactgtcg tgg 33

<210> 28
<211> 64
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<213> Artificial Sequence

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<223> Description of Artificial Sequence:primer

<400> 28
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cata 64

<210> 29
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<212> DNA
<213> Artificial Sequence

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<400> 29
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agctcgcgat 70

<210> 30
<211> 60
<212> DNA
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<211> 60
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<213> Artificial Sequence

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<400> 31

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<211> 21

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:primer

<400> 32

catggatgcg tagttaagcc t 21

<210> 33

<211> 21

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:primer

<400> 33

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<210> 34

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<212> DNA

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<210> 35

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<212> DNA

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agctcgtaca tg 72

<210> 36
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<210> 37
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<400> 37
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<210> 38
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<210> 39
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<400> 39
cagcgaactc gagcaaagtg 20

<210> 40
<211> 79
<212> DNA
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<400> 40
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caagggtctt gttgtagac 79

<210> 41
<211> 28
<212> DNA
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<220>
<223> Description of Artificial Sequence:primer

<400> 41
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<210> 42
<211> 30
<212> DNA
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ggtgtgtggg gatccatgga agaggctttg 30

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<211> 44
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<220>
<223> Description of Artificial Sequence:primer

<400> 43
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<210> 44
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 44
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<210> 45
<211> 37
<212> DNA
<213> Artificial Sequence

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<223> Description of Artificial Sequence:primer

<400> 45
agcaactgct agcttatatt tcatcatccc aaagatc 37

<210> 46
<211> 42
<212> DNA
<213> Artificial Sequence

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<223> Description of Artificial Sequence:primer

<400> 46
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<210> 47
<211> 39
<212> DNA
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<210> 48
<211> 23
<212> DNA
<213> Artificial Sequence

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<223> Description of Artificial Sequence:primer

<400> 48
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<210> 49
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<210> 50
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<220>
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<400> 50
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<210> 51
<211> 78
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<400> 51
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atggaagagg ctttgaga 78

<210> 52
<211> 25
<212> DNA
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<400> 52
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<210> 53
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<400> 53
gggagtcctg cagctcttgt gaac 24

<210> 54
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agctgcatc gcaagcttgg taccgggaat tctctaga 38

<210> 55
<211> 42
<212> DNA
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aatttctaga gaattcccg taccagctt gcttgcgatc gc 42

<210> 56
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<400> 56
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<210> 57
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<220>
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<400> 57
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<210> 58
<211> 22
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<220>
<223> Description of Artificial Sequence:primer

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<210> 59

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 59

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39